RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/736,936A_

Source: _1Fw16_

Date Processed by STIC: _7/27/06_

ENTERED

RAW SEQUENCE LISTING   DATE: 07/27/2006
PATENT APPLICATION: **US/10/736,936A**   TIME: 10:32:16

Input Set : **A:\Amended_SL.ST25.txt**
Output Set: **N:\CRF4\07272006\J736936A.raw**

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 3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: Novel Organic Anion Transport Proteins
 7 <130> FILE REFERENCE: DB23 DIV1
 9 <140> CURRENT APPLICATION NUMBER: US 10/736,936A
10 <141> CURRENT FILING DATE: 2003-12-16
12 <150> PRIOR APPLICATION NUMBER: US 09/575,081
13 <151> PRIOR FILING DATE: 2000-05-19
15 <150> PRIOR APPLICATION NUMBER: US 60/135,081
16 <151> PRIOR FILING DATE: 1999-05-20
18 <160> NUMBER OF SEQ ID NOS: 29
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2830
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (135)..(2207)
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33 cggacgcgtg ggcggacgcg tgggtcgccc acgcgtccga cttgttgcag ttgctgtagg    60
35 attctaaatc caggtgattg tttcaaactg agcatcaaca acaaaaacat ttgtatgata   120
37 tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag    170
38                Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu
39                 1               5                   10
41 gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag    218
42 Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys
43          15                  20                  25
45 atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt    266
46 Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly
47      30                  35                  40
49 gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag    314
50 Ala Ile Ile Met Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu
51 45                  50                  55                  60
53 ata tcc tct tct ctt gtt ggt ttt att gac gga agc ttt gaa att gga    362
54 Ile Ser Ser Ser Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly
55                  65                  70                  75
57 aat ttg ctt gtg att gta ttt gtg agt tac ttt gga tcc aaa cta cat    410
58 Asn Leu Leu Val Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His
59              80                  85                  90
61 aga cca aag tta att gga atc ggt tgt ttc att atg gga att gga ggt    458
62 Arg Pro Lys Leu Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly
63          95                  100                 105
65 gtt ttg act gct ttg cca cat ttc ttc atg gga tat tac agg tat tct    506
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 66 Val Leu Thr Ala Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser
 67      110                 115                 120
 69 aaa gaa act aat atc gat tca tca gaa aat tca aca tcg acc tta tcc      554
 70 Lys Glu Thr Asn Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser
 71 125                 130                 135                 140
 73 act tgt tta att aat caa att tta tca ctc aat aga gca tca cct gag      602
 74 Thr Cys Leu Ile Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu
 75               145                 150                 155
 77 ata gtg gga aaa ggt tgt tta aag gaa tct ggg tca tac atg tgg ata      650
 78 Ile Val Gly Lys Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile
 79              160                 165                 170
 81 tat gtg ttc atg ggt aat atg ctt cgt gga ata ggg gag act ccc ata      698
 82 Tyr Val Phe Met Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile
 83         175                 180                 185
 85 gta cca ttg ggg ctt tct tac att gat gat ttc gct aaa gaa gga cat      746
 86 Val Pro Leu Gly Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His
 87         190                 195                 200
 89 tct tct ttg tat tta ggt ata ttg aat gca ata gca atg att ggt cca      794
 90 Ser Ser Leu Tyr Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro
 91 205                 210                 215                 220
 93 atc att ggc ttt acc ctg gga tct ctg ttt tct aaa atg tac gtg gat      842
 94 Ile Ile Gly Phe Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp
 95              225                 230                 235
 97 att gga tat gta gat cta agc act atc agg ata act cct act gat tct      890
 98 Ile Gly Tyr Val Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser
 99              240                 245                 250
101 cga tgg gtt gga gct tgg tgg ctt aat ttc ctt gtg tct gga cta ttc      938
102 Arg Trp Val Gly Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe
103              255                 260                 265
105 tcc att att tct tcc ata cca ttc ttt ttc ttg ccc caa act cca aat      986
106 Ser Ile Ile Ser Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn
107         270                 275                 280
109 aaa cca caa aaa gaa aga aaa gct tca ctg tct ttg cat gtg ctg gaa     1034
110 Lys Pro Gln Lys Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu
111 285                 290                 295                 300
113 aca aat gat gaa aag gat caa aca gct aat ttg acc aat caa gga aaa     1082
114 Thr Asn Asp Glu Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys
115              305                 310                 315
117 aat att acc aaa aat gtg act ggt ttt ttc cag tct ttt aaa agc atc     1130
118 Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile
119              320                 325                 330
121 ctt act aat ccc ctg tat gtt atg ttt gtg ctt ttg acg ttg tta caa     1178
122 Leu Thr Asn Pro Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln
123              335                 340                 345
125 gta agc agc tat att ggt gct ttt act tat gtc ttc aaa tac gta gag     1226
126 Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu
127         350                 355                 360
129 caa cag tat ggt cag cct tca tct aag gct aac atc tta ttg gga gtc     1274
130 Gln Gln Tyr Gly Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val
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131 365                    370                    375                    380
133 ata acc ata cct att ttt gca agt gga atg ttt tta gga gga tat atc     1322
134 Ile Thr Ile Pro Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile
135                    385                    390                    395
137 att aaa aaa ttc aaa ctg aac acc gtt gga att gcc aaa ttc tca tgt     1370
138 Ile Lys Lys Phe Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys
139                    400                    405                    410
141 ttt act gct gtg atg tca ttg tcc ttt tac cta tta tat ttt ttc ata     1418
142 Phe Thr Ala Val Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile
143                    415                    420                    425
145 ctc tgt gaa aac aaa tca gtt gcc gga cta acc atg acc tat gat gga     1466
146 Leu Cys Glu Asn Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly
147         430                    435                    440
149 aat aat cca gtg aca tct cat aga gat gta cca ctt tct tat tgc aac     1514
150 Asn Asn Pro Val Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn
151 445                    450                    455                    460
153 tca gac tgc aat tgt gat gaa agt caa tgg gaa cca gtc tgt gga aac     1562
154 Ser Asp Cys Asn Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn
155                    465                    470                    475
157 aat gga ata act tac atc tca ccc tgt cta gca ggt tgc aaa tct tca     1610
158 Asn Gly Ile Thr Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser
159                    480                    485                    490
161 agt ggc aat aaa aag cct ata gtg ttt tac aac tgc agt tgt ttg gaa     1658
162 Ser Gly Asn Lys Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu
163         495                    500                    505
165 gta act ggt ctc cag aac aga aat tac tca gcc cat ttg ggt gaa tgc     1706
166 Val Thr Gly Leu Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys
167 510                    515                    520
169 cca aga gat gat gct tgt aca agg aaa ttt tac ttt ttt gtt gca ata     1754
170 Pro Arg Asp Asp Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile
171 525                    530                    535                    540
173 caa gtc ttg aat tta ttt ttc tct gca ctt gga ggc acc tca cat gtc     1802
174 Gln Val Leu Asn Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val
175                    545                    550                    555
177 atg ctg att gtt aaa att gtt caa cct gaa ttg aaa tca ctt gca ctg     1850
178 Met Leu Ile Val Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu
179         560                    565                    570
181 ggt ttc cac tca atg gtt ata cga gca cta gga gga att cta gct cca     1898
182 Gly Phe His Ser Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro
183         575                    580                    585
185 ata tat ttt ggg gct ctg att gat aca acg tgt ata aag tgg tcc acc     1946
186 Ile Tyr Phe Gly Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr
187 590                    595                    600
189 aac aac tgt ggc aca cgt ggg tca tgt agg aca tat aat tcc aca tca     1994
190 Asn Asn Cys Gly Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser
191 605                    610                    615                    620
193 ttt tca agg gtc tac ttg ggc ttg tct tca atg tta aga gtc tca tca     2042
194 Phe Ser Arg Val Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser
195                    625                    630                    635
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197 ctt gtt tta tat att ata tta att tat gcc atg aag aaa aaa tat caa      2090
198 Leu Val Leu Tyr Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln
199         640             645             650
201 gag aaa gat atc aat gca tca gaa aat gga agt gtc atg gat gaa gca      2138
202 Glu Lys Asp Ile Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala
203         655             660             665
205 aac tta gaa tcc tta aat aaa aat aaa cat ttt gtc cct tct gct ggg      2186
206 Asn Leu Glu Ser Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly
207         670             675             680
209 gca gat agt gaa aca cat tgt taagggggaga aaaaaagcca cttctgcttc        2237
210 Ala Asp Ser Glu Thr His Cys
211 685                 690
213 tgtgtttcca aacagcattg cattgattca gtaagatgtt atttttgagg agttcctggt    2297
215 cctttcacta agaatttcca catcttttat ggtggaagta taaataagcc tatgaactta    2357
217 taataaaaca aactgtaggt agaaaaaatg agagtactca ttgttacatt atagctacat    2417
219 atttgtggtt aaggttagac tatatgatcc atacaaatta aagtgagaga catggttact    2477
221 gtgtaataaa agaaaaaata cttgttcagg taattctaat tcttaataaa acaaatgagt    2537
223 atcatacagg tagaggttaa aaaggaggag ctagattcat atcctaagta aagagaaatg    2597
225 cctagtgtct atttttattaa acaaacaaac acagagtttg aactataata ctaaggcctg   2657
227 aagtctagct tggatatatg ctacaataat atctgttact cacataaaat tatatatttc    2717
229 acagacttta tcaatgtata attaacaatt atcttgttta agtaaattta gaatacattt    2777
231 aagtattgtg gaagaaataa agacattcca atatttgcaa aaaaaaaaaa aaa           2830
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 691
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 2
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245 Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
246         20              25              30
249 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
250         35              40              45
253 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
254     50              55              60
257 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
258 65              70              75              80
261 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
262         85              90              95
265 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
266         100             105             110
269 Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
270         115             120             125
273 Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
274     130             135             140
277 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
278 145             150             155             160
281 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
282             165             170             175
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285 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
286             180             185             190
289 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
290         195             200             205
293 Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
294         210             215             220
297 Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
298 225             230             235             240
301 Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
302             245             250             255
305 Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
306             260             265             270
309 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
310         275             280             285
313 Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
314         290             295             300
317 Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
318 305             310             315             320
321 Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
322             325             330             335
325 Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
326         340             345             350
329 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
330         355             360             365
333 Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
334         370             375             380
337 Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
338 385             390             395             400
341 Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
342             405             410             415
345 Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
346             420             425             430
349 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
350             435             440             445
353 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
354         450             455             460
357 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
358 465             470             475             480
361 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
362             485             490             495
365 Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
366             500             505             510
369 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
370         515             520             525
373 Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
374         530             535             540
377 Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val
378 545             550             555             560
381 Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/27/2006
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Input Set : **A:\Amended_SL.ST25.txt**
Output Set: **N:\CRF4\07272006\J736936A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 33,594
Seq#:8; Xaa Pos. 33,594

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:29

VERIFICATION SUMMARY   DATE: 07/27/2006
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Input Set : **A:\Amended_SL.ST25.txt**
Output Set: **N:\CRF4\07272006\J736936A.raw**

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L:1241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:748
L:1381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2428
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592
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